

AGCATCCTGA GTAATGAGTG GCCTGGGCCG GAGCAGGCCG GGTGGCCGGA GCCGTGTGGA	60
CCAGGAGGAG CCCTTTCCAC AGGGCCTGTG GACGGGGGTG GCTATGAGAT CCTGCCCCGA	120
AGAGCAGTAC TGGGATCCTC TGCTGGGTAC CTGCATGTCC TGCAAAACCA TTTGCAACCA	180
TCAGAGCCAG CGCACCTGTG CAGCCTTCTG CAGGTCACTC AGCTGCCGCA AGGAGCAAGG	240
CAAGTTCTAT GACCATCTCC TGAGGGACTG CATCAGCTGT GCCTCCATCT GTGGACAGCA	300
CCCTAAGCAA TGTGCATACT TCTGTGAGAA CAAGCTCAGG AGCCCAGTGA ACCTTCCACC	360
AGAGCTCAGG AGACAGCGGA GTGGAGAAGT TGAACAAT TCAGACAAC TCGGAAGGTA	420
CCAAGGATTG GAGCAGAG GCTCAGAAGC AAGTCCAGCT CTCCCGGGC TGAAGCTGAG	480
TGCAGATCAG GTGGCCCTGG TCTACAGCAC GCTGGGGCTC TGCCTGTGTG CCGTCTCTG	540
CTGCTTCCTG GTGGCGGTGG CCTGCTTCTT CAAGAAGAGG GGGGATCCCT GCTCCTGCCA	600
GCCCCGCTCA AGGCCCCGTC AAGTCCGGC CAAGTCTTCC CAGGATCAG CGATGGAAGC	660
CGGCAGCCCT GTGAGCACAT CCCCCGAGCC AGTGGAGACC TGCAGCTTCT GCTTCCCTGA	720
GTGCAGGGCG CCCACGCAGG AGAGCGCAGT CACGCCTGGG ACCCCCGACC CCACTTGTGC	780
TGGAAGGTGG GGGTGCCACA CCAGGACCAC AGTCCTGCAG CCTTGCCCCAC ACATCCCAGA	840
CAGTGGCCTT GGCATTGTGT GTGTGCCTGC CCAGGAGGGG GGCCAGGTG CATAAATGGG	900
GGTCAGGGAG GGAAGGAGG AGGGAGAGAG ATGGAGAGGA GGGGAGAGAG AAAGAGAGGT	960
GGGGAGAGGG GAGAGAGATA TGAGGAGAGA GAGACAGAGG AGGCAGAAAG GGAGAGAAAC	1020
AGAGGAGACA GAGAGGGAGA GAGAGACAGA GGGAGAGAGA GACAGAGGGG AAGAGAGGCA	1080
GAGAGGGAAA GAGGCAGAGA AGGAAAGAGA CAGGCAGAGA AGGAGAGAGG CAGAGAGGGA	1140
GAGAGGCAGA GAGGGAGAGA GGCAGAGAGA CAGAGAGGGA GAGAGGGACA GAGAGAGATA	1200
GAGCAGGAGG TCGGGGCACT CTGAGTCCCA GTTCCAGTG CAGCTGTAGG TCGTCATCAC	1260
CTAACCACAC GTGCAATAAA GTCCTCGTGC CTGCTGCTCA CAGCCCCCGA GAGCCCTCC	1320
TCTGGAGAA TAAACCTTT GGCAGCTGCC CTTCTCAA AAAAAAAAAA AAAAAA	1377

FIGURE 1A

Met Ser Gly Leu Gly Arg Ser Arg Arg Gly Gly Arg Ser Arg Val Asp
 1 5 10 15
 Gln Glu Glu Arg Phe Pro Gln Gly Leu Trp Thr Gly Val Ala Met Arg
 20 25 30
 Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu Gly Thr Cys Met
 35 40 45
 Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg Thr Cys Ala Ala
 50 55 60
 Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp
 65 70 75 80
 His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His
 85 90 95
 Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser Pro Val
 100 105 110
 Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val Glu Asn
 115 120 125
 Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg Gly Ser
 130 135 140
 Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp Gln Val
 145 150 155 160
 Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys Ala Val Leu Cys
 165 170 175
 Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys Arg Gly Asp Pro
 180 185 190
 Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser Pro Ala Lys Ser
 195 200 205
 Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val Ser Thr Ser Pro
 210 215 220
 Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu Cys Arg Ala Pro
 225 230 235 240
 Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp Pro Thr Cys Ala
 245 250 255
 Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu Gln Pro Cys Pro
 260 265 270
 His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val Pro Ala Gln Glu
 275 280 285
 Gly Gly Pro Gly Ala
 290

FIGURE 1B

(start and stop codons are in bold type)

AGCAAGTTCA GCCTGGTTAA GTCCAAGCTG AATTCCGGTC AAAGTTCAAG
TAGTGAT**ATG** GATGACTCCA CAGAAAGGGA GCAGTCACGC CTTACTTCTT
GCCTTAAGAA AAGAGAAGAA ATGAAACTGA AGGAGTGTGT TTCCATCCTC
CCACGGAAGG AAAGCCCCTC TGTCCGATCC TCCAAAGACG GAAAGCTGCT
GGCTGCAACC TTGCTGCTGG CACTGCTGTC TTGCTGCCTC ACGGTGGTGT
CTTTCTACCA GGTGGCCGCC CTGCAAGGGG ACCTGGCCAG CCTCCGGGCA
GAGCTGCAGG GCCACCACGC GGAGAAGCTG CCAGCAGGAG CAGGAGCCCC
CAAGGCCGGC CTGGAGGAAG CTCCAGCTGT CACCGCGGGA CTGAAAATCT
TTGAACCACC AGCTCCAGGA GAAGGCAACT CCAGTCAGAA CAGCAGAAAT
AAGCGTGCCG TTCAGGGTCC AGAAGAAACA GTCACTCAAG ACTGCTTGCA
ACTGATTGCA GACAGTGAAA CACCAACTAT ACAAAAAGGA TCTTACACAT
TTGTTCCATG GCTTCTCAGC TTTAAAAGGG GAAGTGCCCT AGAAGAAAAA
GAGAATAAAA TATTGGTCAA AGAAACTGGT TACTTTTTTA TATATGGTCA
GGTTTTATAT ACTGATAAGA CCTACGCCAT GGGACATCTA ATTCAGAGGA
AGAAGGTCCA TGTCTTTGGG GATGAATTGA GTCTGGTGAC TTTGTTTCGA
TGTATTCAAA ATATGCCTGA AACACTACCC AATAATTCCT GCTATTCAGC
TGGCATTGCA AACTGGAAG AAGGAGATGA ACTCCAATT GCAATACCAA
GAGAAAATGC ACAAATATCA CTGGATGGAG ATGTCACATT TTTTGGTGCA
TTGAAACTGC TGT**G**ACCTAC TTACACCATG TCTGTAGCTA TTTTCCTCCC
TTTCTCTGTA CCTCTAAGAA GAAAGAATCT AACTGAAAAT ACCAAAAAAA
AAAAAAAAAA AAAAAGATCT TTAATTAAGC GGCCGCAAGC TTATTCCCTT
TAGTGAG

FIGURE 2A

Translation in relevant reading frame (3' 5'):

MDDSTEREQS	RLTSCLKKRE	EMKLKECVSI	LPRKESPSVR	SSKDGKLLAA
TLLLALLSCC	LTVVSFYQVA	ALQGDLASLR	AELQGHHA EK	LPAGAGAPKA
GLEEAPAVTA	GLKIFEPPAP	GEGNSSQNSR	NKRAVQGPEE	TVTQDCLQLI
ADSETPTIQK	GSYTFVPWLL	SFKRGSAL EE	KENKILVKET	GÝFFIYGQVL
YTDKTYAMGH	LIQRKKVHVF	GDELSLVTLF	RCIQNMPETL	PNNSCYSAGI
AKLEEĞDELQ	LAIPRENAQI	SLDGDVTFFG	ALKLL	

FIGURE 2B

Translation in relevant reading frame (3' 5'):

MARRLWILSL LAVTLTVALA APSQKSKRRT SSDRMKQIED KIEEILSKIY
HIENEIARIK KLIGERTRSG NSSQNSRNKR AVQGPEETVT QDCLQLIADS
ETPTIQKGSY TFVPWLLSFK RGSALEEKEN KILVKETGYF FIYGQVLYTD
KTYAMGHLIQ RKKVHVFGDE LSLVTLFRCI QNMPETLPNN SCYSAGIAKL
EEGDELQLAI PRENAQISLD GDVTFFGALK LL
(SEQ ID NO:3)

FIGURE 3

1, 2 d.h.
Plate Binding assay-NLLZ + HuTACIFc (Goat anti-human Fc) 1/6/99
25-FEB-99

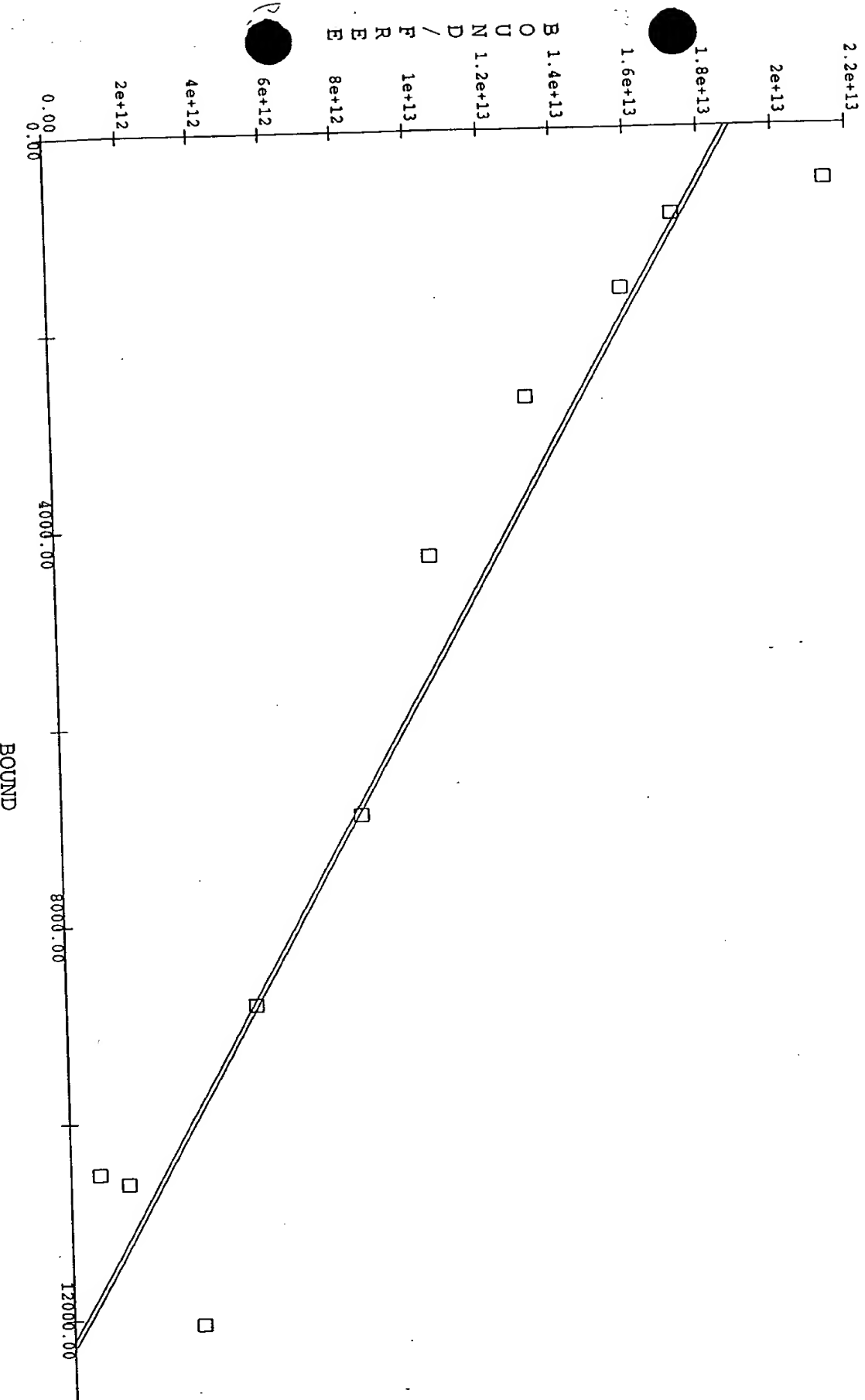
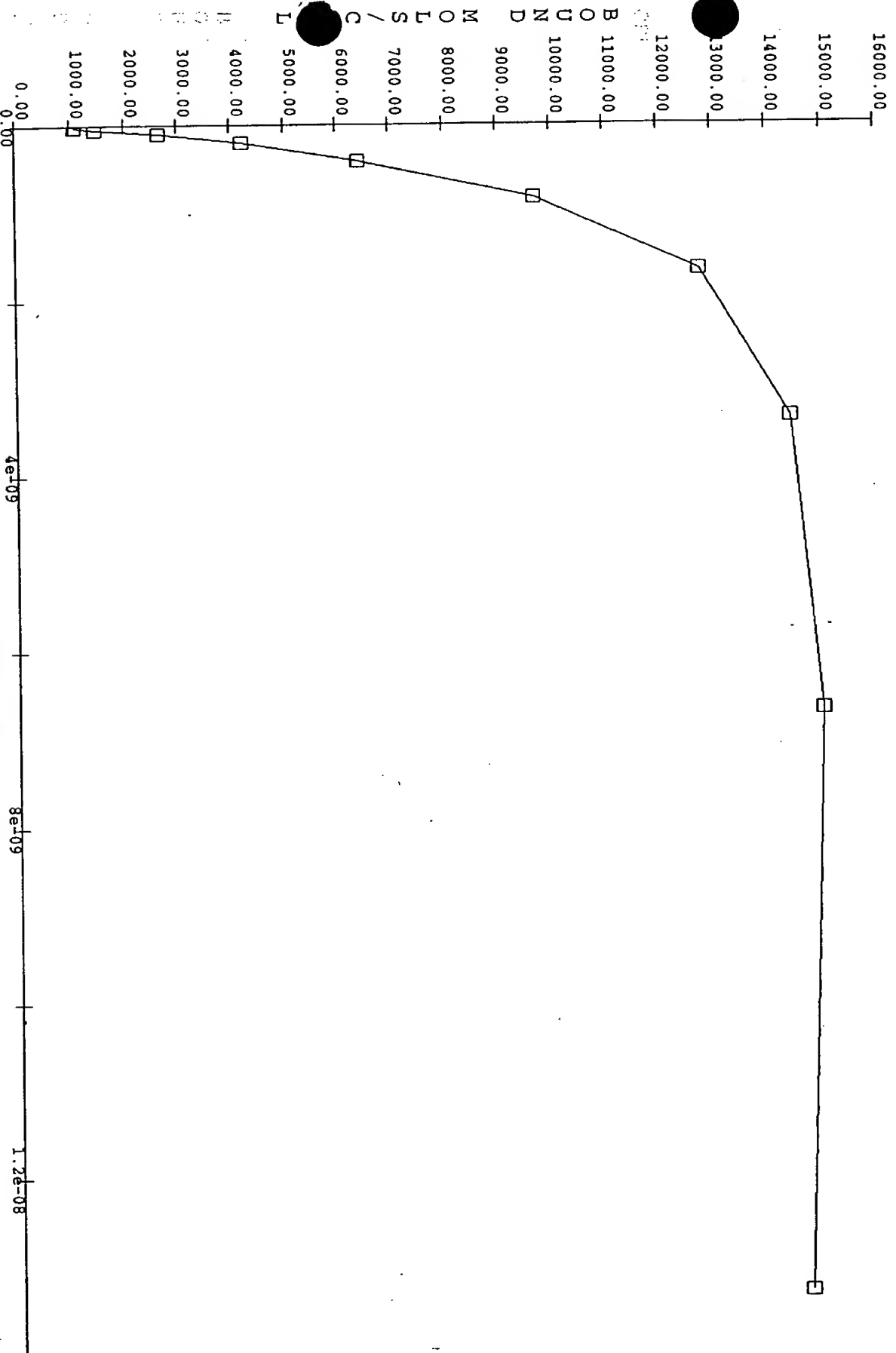


FIGURE 4B

1:5 d_{1/2}
Plate Binding assay-NLLZ + HuTACIFc (Goat anti-hu Fc) 1/6/99 duplicate
25-FEB-99



100000 FREE CONCENTRATION

FIGURE 5A

1:5 d.h.
Plate Binding assay-NLLZ + HuTACIFC (Goat anti-hu Fc) 1/6/99 duplicate
25-FEB-99

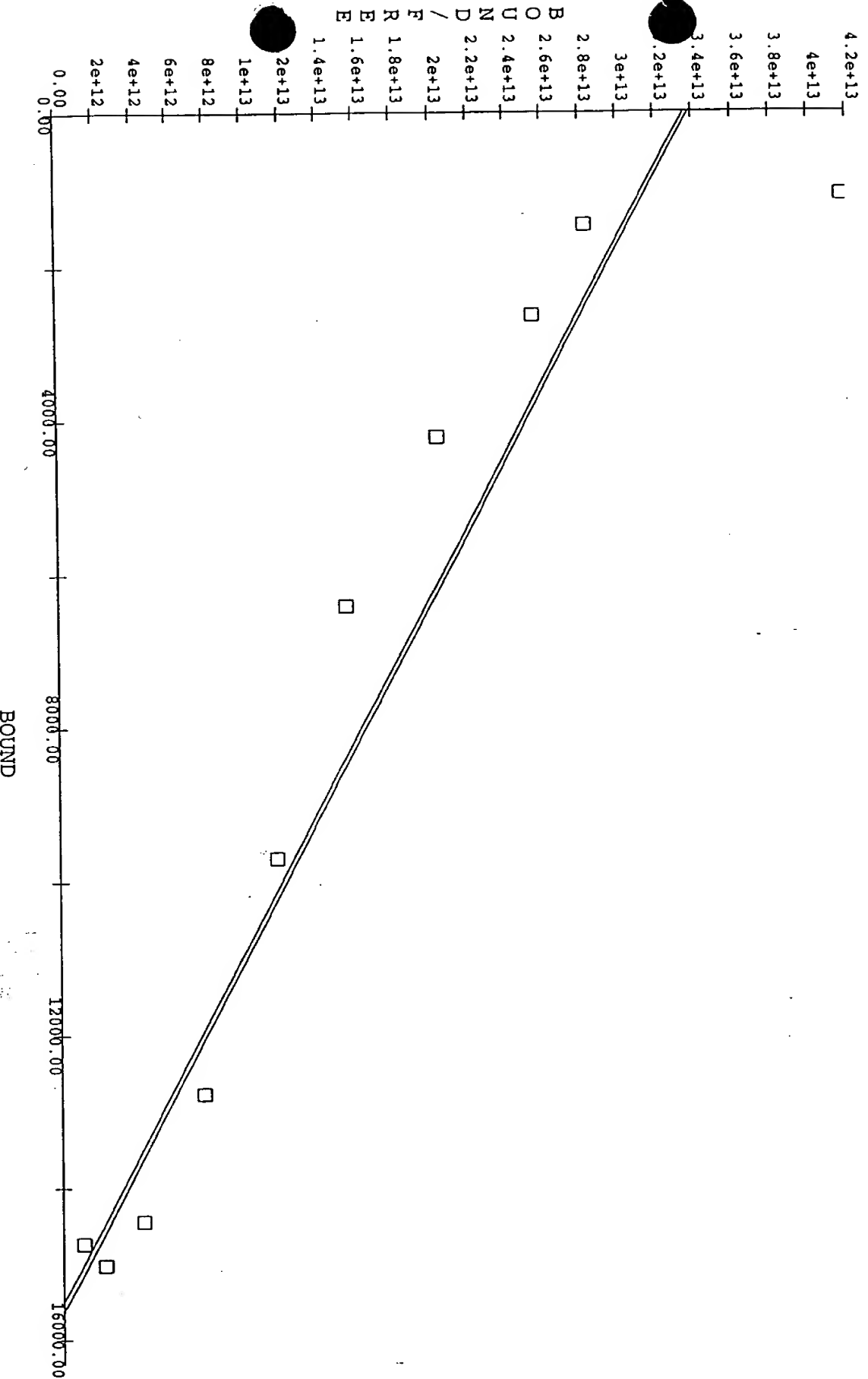
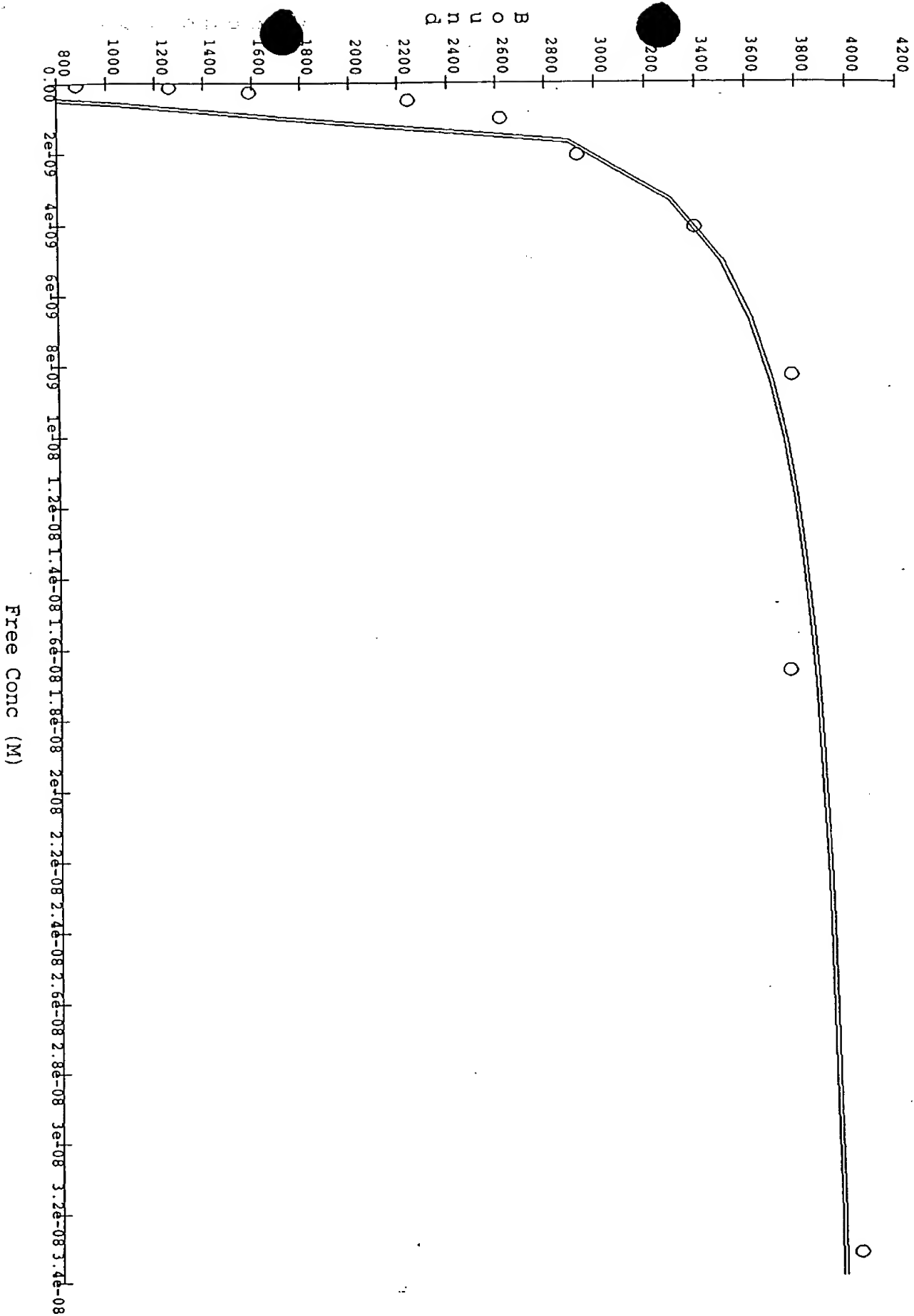
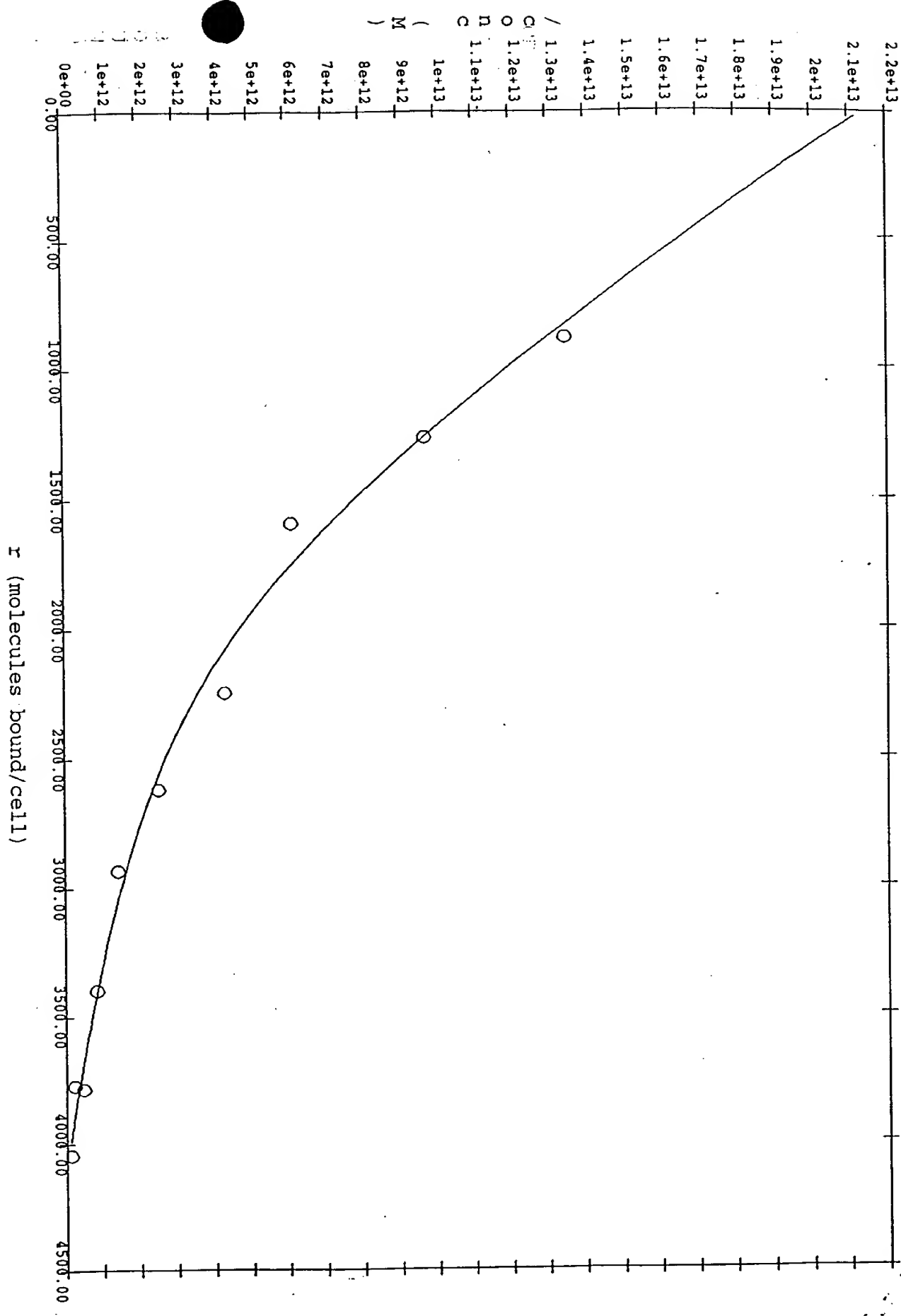


FIGURE 5B



○ Data points
 (2.1e+03*5.7e+08*X) / (1+5.7e+08*X) + (1.9e+03*1.0e+10*X) / (1+1.0e+10*X)

FIGURE 6A



○ Data points
 (2.1e+03*5.7e+08*X)/(1+5.7e+08*X)+(1.9e+03*1.0e+10*X)/(1+1.0e+10*X)

00302253.043000

FIGURE 6B